AUTHORS Du,X., Poltorak,A., Wei,Y. and Beutler,B.
TITLE Three novel mammalian toll-like receptors: gene structure, expression, and evolution
JOURNAL Eur. Cytokine Netw. 11 (3), 362-371 (2000)
PUBMED 11022119
REFERENCE 7 (residues 1 to 1049)
AUTHORS Rock,F.L., Hardiman,G., Timans,J.C., Kastelein,R.A. and Bazan,J.F.
TITLE A family of human receptors structurally related to Drosophila Toll
JOURNAL Proc. Natl. Acad. Sci. U.S.A. 95 (2), 588-593 (1998)
PUBMED 9435236
COMMENT REVIEWED REFSEQ: This record has been curated by NCBI staff. The reference sequence was derived from AF245702.1 and AF240467.1.

Summary: The protein encoded by this gene is a member of the Toll-like receptor (TLR) family which plays a fundamental role in pathogen recognition and activation of innate immunity. TLRs are highly conserved from Drosophila to humans and share structural and functional similarities. They recognize pathogen-associated molecular patterns (PAMPs) that are expressed on infectious agents, and mediate the production of cytokines necessary for the development of effective immunity. The various TLRs exhibit different patterns of expression. This gene is predominantly expressed in lung, placenta, and spleen, and lies in close proximity to another family member, TLR8, on chromosome X.

FEATURES Location/Qualifiers
source 1..1049
/organism="Homo sapiens"
/db_xref="taxon:9606"
/chromosome="X"
/map="Xp22.3"
Protein 1..1049
/product="toll-like receptor 7"
variation 11
/replace="Q"
/replace="L"
/db_xref="dbSNP:179008"
Region <75..>423
/region_name="Membrane glycoprotein LIG-1 [Signal transduction mechanisms]"
/note="KOG4194"
/db_xref="CDD:21971"
Region 256..768
/region_name="Extracellular matrix protein slit, contains leucine-rich and EGF-like repeats [Extracellular structures, Signal transduction mechanisms]"
/note="KOG4237"
/db_xref="CDD:22013"
Region 319..>833
/region_name="Membrane glycoprotein LIG-1 [Signal transduction mechanisms]"
/note="KOG4194"
/db_xref="CDD:21971"
variation 448
/replace="A"
/replace="V"
/db_xref="dbSNP:5743781"
Region 498..>654
/region_name="Ras suppressor protein (contains

```
                     /note="KOG4579"
                     /db_xref="CDD:22354"
     Region          893..1034
                     /region_name="TIR domain"
                     /note="TIR"
                     /db_xref="CDD:23237"
     CDS             1..1049
                     /gene="TLR7"
                     /coded_by="NM_016562.2:136..3285"
                     /note="go_component: integral to membrane [goid 0016021]
                     [evidence IEA];
                     go_function: transmembrane receptor activity [goid
                     0004888] [evidence IEA];
                     go_process: immune response [goid 0006955] [evidence IEA];
                     go_process: inflammatory response [goid 0006954] [evidence
                     IEA]"
                     /db_xref="GeneID:51284"
                     /db_xref="LocusID:51284"
                     /db_xref="MIM:300365"
ORIGIN
        1 mvfpmwtlkr qililfniil iskllgarwf pktlpcdvtl dvpknhvivd ctdkhlteip
       61 ggiptnttnl tltinhipdi spasfhrldh lveidfrcnc vpiplgsknn mcikrlqikp
      121 rsfsgltylk slyldgnqll eipqglppsl qllsleanni fsirkenlte lanieilylg
      181 qncyyrnpcy vsysiekdaf lnltklkvls lkdnnvtavp tvlpstltel ylynnmiaki
      241 qeddfnnlnq lqildlsgnc prcynapfpc apcknnsplq ipvnafdalt elkvlrlhsn
      301 slqhvpprwf kninklqeld lsqnflakei gdakflhflp sliqldlsfn felqvyrasm
      361 nlsqafsslk slkilrirgy vfkelksfnl splhnlqnle vldlgtnfik ianlsmfkqf
      421 krlkvidlsv nkispsgdss evgfcsnart svesyepqvl eqlhyfrydk yarscrfknk
      481 easfmsvnes cykygqtldl sknsiffvks sdfqhlsflk clnlsgnlis qtlngsefqp
      541 laelryldfs nnrldllhst afeelhklev ldissnshyf qsegithmln ftknlkvlqk
      601 lmmndndiss stsrtmeses lrtlefrgnh ldvlwregdn rylqlfknll kleeldiskn
      661 slsflpsgvf dgmppnlknl slaknglksf swkklqclkn letldlshnq lttvperlsn
      721 csrslknlil knnqirsltk yflqdafqlr yldlssnkiq miqktsfpen vlnnlkmlll
      781 hhnrflctcd avwfvwwvnh tevtipylat dvtcvgpgah kgqsvisldl ytceldltnl
      841 ilfslsisvs lflmvmmtas hlyfwdvwyi yhfckakikg yqrlispdcc ydafivydtk
      901 dpavtewvla elvakledpr ekhfnlclee rdwlpgqpvl enlsqsiqls kktvfvmtdk
      961 yaktenfkia fylshqrlmd ekvdviilif lekpfqkskf lqlrkrlcgs svlewptnpq
     1021 ahpyfwqclk nalatdnhva ysqvfketv
//
```

Sequence